



10/530844

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SEQUENCE LISTING

<110> Consortium für elektrochemische Industrie GmbH

<120> Feedback-resistant homoserine-Transsuccinylases having a modified C-terminus

<130> Co10221

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<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

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<221> CDS

<222> (1)..(930)

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<305> 533

<306> 1453-1474

<307> 1997

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atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt 48

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

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gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa 96

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20 25 30

att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att 144  
Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile  
35 40 45

gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag 192  
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln  
50 55 60

gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg 240  
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr  
65 70 75 80

ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag 288  
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln  
85 90 95

gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg 336  
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu  
100 105 110

gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg 384  
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu  
115 120 125

gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg 432  
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala  
130 135 140

gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc 480  
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg  
145 150 155 160

acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat 528  
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His  
165 170 175

gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg 576  
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser  
180 185 190

cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg 624  
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu  
195 200 205

gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt 672  
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser  
210 215 220

aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg 720  
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala  
225 230 235 240

caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac 768  
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp  
245 250 255

ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca 816  
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr  
260 265 270

ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg 864  
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp  
275 280 285

ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg 912  
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290 295 300

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Asn Pro Thr Leu Asp  
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Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu  
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Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile  
35 40 45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

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 Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr  
 65                      70                      75                      80  
 Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln  
 85                      90                      95  
 Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu  
 100                      105                      110  
 Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu  
 115                      120                      125  
 Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala  
 130                      135                      140  
 Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg  
 145                      150                      155                      160  
 Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His  
 165                      170                      175  
 Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser  
 180                      185                      190  
 Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu  
 195                      200                      205  
 Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser  
 210                      215                      220  
 Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala  
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 Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp  
 245                      250                      255  
 Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr  
 260                      265                      270  
 Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp  
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Asn Pro Thr Leu Asp  
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<223> Description of Artificial Sequence: Primer for PCR

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<223> Description of Artificial Sequence:      Primer for PCR

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<223> Description of Artificial Sequence: Primer for PCR

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<223> Description of Artificial Sequence: Changes in Met A structural gene

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Changes in Protein encoded by altered Met A structural gene

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Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly

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<211> 102

<212> DNA

<213> Artificial Sequence

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Changes in protein encoded by altered Met A structural gene

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Ser Tyr Ile His Gln Tyr Leu Leu Val Asn Asn Ser Thr Glu Leu Trp

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Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly

20 25 30

Gly Ala